



HQ
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SEQUENCE LISTING

<110> Macrozyme
Aerts, Johannes M.F.G.
Boot, Rolf G.

<120> A mammalian mucinase, its recombinant production, and its use in therapy or prophylaxis against diseases in which mucus is involved or infection diseases

<130> 2183-5136US

<140> 10/004,219
<141> 2001-11-02

<160> 14

<170> PatentIn Ver. 2.1

<210> 1
<211> 476
<212> PRT
<213> Artificial Sequence

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amino acid sequence deduced from cDNA sequence

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Gln Leu Gly Ser Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala
20 25 30

Gln Tyr Arg Pro Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro
35 40 45

Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn
50 55 60

Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe
65 70 75 80

Asn Gly Leu Lys Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile
85 90 95

Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr
100 105 110

Pro Glu Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg
115 120 125

Gln Tyr Glu Phe Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser
130 135 140

Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln
145 150 155 160

Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro
165 170 175

Arg Leu Met Val Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln
180 185 190

Ser Gly Tyr Glu Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His
195 200 205

Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu
210 215 220

Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr
225 230 235 240

Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro
245 250 255

Ala Glu Lys Leu Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile
260 265 270

Leu Ser Asn Pro Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala
275 280 285

Gly Pro Ala Gly Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr
290 295 300

Glu Ile Cys Thr Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala
305 310 315 320

Pro Gln Glu Val Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr
325 330 335

Asp Asn Ile Lys Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn
340 345 350

Lys Phe Gly Gly Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr
355 360 365

Gly Thr Phe Cys Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys
370 375 380

Lys Ala Leu Gly Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro
385 390 395 400

Ile Glu Pro Ile Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly
405 410 415

Ser Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val
420 425 430

Arg Ala Asn Gly Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp
435 440 445

His Cys Val Asn Gly Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu
450 455 460

Val Phe Asp Thr Ser Cys Asp Cys Cys Asn Trp Ala
465 470 475

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AMCase cDNA sequence and deduced amino acid
sequence

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cDNA sequence and deduced amino acid sequence

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Met Thr Lys Leu
1

att ctc ctc aca ggt ctt gtc ctt ata ctg aat ttg cag ctc ggc tct 163
Ile Leu Leu Thr Gly Leu Val Leu Ile Leu Asn Leu Gln Leu Gly Ser
5 10 15 20

gcc tac cag ctg aca tgc tac ttc acc aac tgg gcc cag tac cgg cca 211
Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala Gln Tyr Arg Pro
25 30 35

ggc ctg ggg cgc ttc atg cct gac aac atc gac ccc tgc ctc tgt acc 259
Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro Cys Leu Cys Thr
40 45 50

cac ctg atc tac gcc ttt gct ggg agg cag aac aac gag atc acc acc 307
His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn Glu Ile Thr Thr
55 60 65

atc gaa tgg aac gat gtg act ctc tac caa gct ttc aat ggc ctg aaa 355
Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe Asn Gly Leu Lys
70 75 80

aat aag aac agc cag ctg aaa act ctc ctg gcc att gga ggc tgg aac 403
Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn
85 90 95 100

ttc ggg act gcc cct ttc act gcc atg gtt tct act cct gag aac cgc 451
Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr Pro Glu Asn Arg
105 110 115

cag act ttc atc acc tca gtc atc aaa ttc ctg cgc cag tat gag ttt 499
Gln Thr Phe Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Glu Phe
120 125 130

gac ggg ctg gac ttt gac tgg gag tac cct ggc tct cgt ggg agc cct 547
Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro
135 140 145

cct cag gac aag cat ctc ttc act gtc ctg gtg cag gaa atg cgt gaa 595
Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln Glu Met Arg Glu

150	155	160	
gct ttt gag cag gag gcc aag cag atc aac aag ccc agg ctg atg gtc Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro Arg Leu Met Val			643
165	170	175	180
act gct gca gta gct gct ggc atc tcc aat atc cag tct ggc tat gag Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln Ser Gly Tyr Glu			691
185	190		195
atc ccc caa ctg tca cag tac ctg gac tac atc cat gtc atg acc tac Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His Val Met Thr Tyr			739
200	205		210
gac ctc cat ggc tcc tgg gag ggc tac act gga gag aac agc ccc ctc Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu			787
215	220		225
tac aaa tac ccg act gac acc ggc agc aac gcc tac ctc aat gtg gat Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp			835
230	235		240
tat gtc atg aac tac tgg aag gac aat gga gca cca gct gag aag ctc Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro Ala Glu Lys Leu			883
245	250		255
260			
atc gtt gga ttc cct acc tat gga cac aac ttc atc ctg agc aac ccc Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile Leu Ser Asn Pro			931
265	270		275
tcc aac act gga att ggt gcc ccc acc tct ggt gct cct gct ggg Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala Gly Pro Ala Gly			979
280	285		290
ccc tat gcc aag gag tct ggg atc tgg gct tac tac gag atc tgt acc Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr Glu Ile Cys Thr			1027
295	300		305
ttc ctg aaa aat gga gcc act cag gga tgg gat gcc cct cag gaa gtg Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala Pro Gln Glu Val			1075
310	315		320
cct tat gcc tat cag ggc aat gtg tgg gtt ggc tat gac aac atc aag Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr Asp Asn Ile Lys			1123
325	330		335
340			
agc ttc gat att aag gct caa tgg ctt aag cac aac aaa ttt gga ggc Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn Lys Phe Gly Gly			1171
345	350		355
gcc atg gtc tgg gcc att gat ctg gat gac ttc act ggc act ttc tgc Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Thr Phe Cys			1219
360	365		370
aac cag ggc aag ttt ccc cta atc tcc acc ctg aag aag gcc ctc ggc Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys Lys Ala Leu Gly			1267
375	380		385
ctg cag agt gca agt tgc acg gct cca gct cag ccc att gag cca ata Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro Ile Glu Pro Ile			1315
390	395		400

act gct gct ccc agt ggc agc ggg aac ggg agc ggg agt agc agc tct	1363
Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly Ser Ser Ser Ser	
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gga ggc agc tcg gga ggc agt gga ttc tgt gct gtc aga gcc aac ggc	1411
Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val Arg Ala Asn Gly	
425 430 435	
ctc tac ccc gtg gca aat aac aga aat gcc ttc tgg cac tgc gtg aat	1459
Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp His Cys Val Asn	
440 445 450	
gga gtc acg tac cag cag aac tgc cag gcc ggg ctt gtc ttc gac acc	1507
Gly Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu Val Phe Asp Thr	
455 460 465	
agc tgt gat tgc tgc aac tgg gca taaacctgac ctggctata ttccctagag	1561
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agtc	1625

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AMCase cDNA sequence and deduced amino acid	
sequence	
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cDNA sequence and deduced amino acid sequence	
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1 5 10 15	
cag ctg ggg tct gcc tac aat ctg ata tgc tat ttc acc aac tgg gcc	96
Gln Leu Gly Ser Ala Tyr Asn Leu Ile Cys Tyr Phe Thr Asn Trp Ala	
20 25 30	
cag tat cgg cca ggt ctg ggg agc ttc aag cct gat gac att aac ccc	144
Gln Tyr Arg Pro Gly Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro	
35 40 45	
tgc ctg tgt act cac ctg atc tat gcc ttt gct ggg atg cag aac aat	192
Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn	
50 55 60	

gag atc acc acc ata gaa tgg aat gat gtt act ctc tat aaa gct ttc Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe 65 70 75 80	240
aat gac ttg aaa aac agg aac agc aaa ctg aaa acc ctc ctg gca att Asn Asp Leu Lys Asn Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile 85 90 95	288
gga ggc tgg aac ttt gga act gct cct ttc act acc atg gtt tcc act Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr 100 105 110	336
tct cag aac cgc cag acc ttc att acc tca gtc atc aaa ttt ctg cgt Ser Gln Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg 115 120 125	384
cag tat ggg ttt gat gga ctg gac ctg gac tgg gaa tac cca ggc tca Gln Tyr Gly Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser 130 135 140	432
cgt ggg agc cct cct cag gac aag cat ctc ttc act gtc ctg gtg aag Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Lys 145 150 155 160	480
gaa atg cgt gaa gct ttt gag cag gag gct att gag agc aac agg ccc Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro 165 170 175	528
aga ctg atg gtt act gct gta gct ggt ggg att tcc aac atc cag Arg Leu Met Val Thr Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln 180 185 190	576
gct ggc tat gag atc cct gaa ctt tct aag tac ctg gat ttc atc cat Ala Gly Tyr Glu Ile Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His 195 200 205	624
gtc atg aca tat gac ctc cat ggc tcc tgg gag ggc tac act ggg gag Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu 210 215 220	672
aat agt cct ctt tac aaa tac cct act gag act ggt agc aat gcc tac Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr 225 230 235 240	720
ctc aat gtg gat tat gtc atg aac tat tgg aag aac aat gga gcc cca Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro 245 250 255	768
gct gag aag ctc att gtt gga ttc cca gag tat gga cac acc ttc atc Ala Glu Lys Leu Ile Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile 260 265 270	816
ctg aga aac ccc tct gat aat gga att ggt gcc cct acc tct ggt gat Leu Arg Asn Pro Ser Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp 275 280 285	864
ggc cct gct ggc gcc tat acc aga cag gct ggg ttc tgg gcc tac tat Gly Pro Ala Gly Ala Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr 290 295 300	912
gag att tgc acc ttt ctg aga agt gga gcc act gag gtc tgg gat gcc	960

Glu Ile Cys Thr Phe Leu Arg Ser Gly Ala Thr Glu Val Trp Asp Ala			
305	310	315	320
tcc caa gaa gtg ccc tat gcc tat aag gcc aac gag tgg ctt ggc tat			1008
Ser Gln Glu Val Pro Tyr Ala Tyr Lys Ala Asn Glu Trp Leu Gly Tyr			
325	330	335	
gac aat atc aag agc ttc agt gtt aag gct cag tgg ctt aag cag aac			1056
Asp Asn Ile Lys Ser Phe Ser Val Lys Ala Gln Trp Leu Lys Gln Asn			
340	345	350	
aat ttt gga ggt gcc atg atc tgg gcc att gac ctt gat gac ttc act			1104
Asn Phe Gly Gly Ala Met Ile Trp Ala Ile Asp Leu Asp Asp Phe Thr			
355	360	365	
ggc tct ttc tgt gat cag gga aaa ttt cct ctg act tct act ttg aac			1152
Gly Ser Phe Cys Asp Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn			
370	375	380	
aaa gcc ctt ggc ata tcc act gaa ggt tgc aca gct cct gac gtg cct			1200
Lys Ala Leu Gly Ile Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro			
385	390	395	400
tcc gag cca gtg act act cct cca gga agt ggg agt ggg ggt gga agc			1248
Ser Glu Pro Val Thr Pro Pro Gly Ser Gly Ser Gly Gly Ser			
405	410	415	
tcc gga gga agc tct gga ggc agt gga ttc tgt gcc gac aaa gca gat			1296
Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp			
420	425	430	
ggc ctc tac cct gtg gca gat gac aga aat gct ttt tgg cag tgc atc			1344
Gly Leu Tyr Pro Val Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile			
435	440	445	
aat gga atc aca tac cag cag cat tgt caa gca ggg ctt gtt ttt gat			1392
Asn Gly Ile Thr Tyr Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp			
450	455	460	
acc agc tgt aat tgc tgc aac tgg cca tgaaccta at gccattcttc			1439
Thr Ser Cys Asn Cys Asn Trp Pro			
465	470		
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atgcaataaa attggtagcc aaaaca			1525

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<211> 473
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amino acid sequence deduced from cDNA sequence

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20 25 30

Gln Tyr Arg Pro Gly Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro
35 40 45

Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn
50 55 60

Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe
65 70 75 80

Asn Asp Leu Lys Asn Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile
85 90 95

Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr
100 105 110

Ser Gln Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg
115 120 125

Gln Tyr Gly Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser
130 135 140

Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Lys
145 150 155 160

Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro
165 170 175

Arg Leu Met Val Thr Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln
180 185 190

Ala Gly Tyr Glu Ile Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His
195 200 205

Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu
210 215 220

Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr
225 230 235 240

Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro
245 250 255

Ala Glu Lys Leu Ile Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile
260 265 270

Leu Arg Asn Pro Ser Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp
275 280 285

Gly Pro Ala Gly Ala Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr
290 295 300

Glu Ile Cys Thr Phe Leu Arg Ser Gly Ala Thr Glu Val Trp Asp Ala
305 310 315 320

Ser Gln Glu Val Pro Tyr Ala Tyr Lys Ala Asn Glu Trp Leu Gly Tyr
325 330 335

Asp Asn Ile Lys Ser Phe Ser Val Lys Ala Gln Trp Leu Lys Gln Asn

340

345

350

Asn Phe Gly Gly Ala Met Ile Trp Ala Ile Asp Leu Asp Asp Phe Thr
355 360 365

Gly Ser Phe Cys Asp Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn
370 375 380

Lys Ala Leu Gly Ile Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro
385 390 395 400

Ser Glu Pro Val Thr Thr Pro Pro Gly Ser Gly Ser Gly Gly Ser
405 410 415

Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp
420 425 430

Gly Leu Tyr Pro Val Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile
435 440 445

Asn Gly Ile Thr Tyr Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp
450 455 460

Thr Ser Cys Asn Cys Cys Asn Trp Pro
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<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: A-tail primer

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<221> misc_feature

<222> (1)..(22)

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<210> 6

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: anti-sense
primer MAS1

<220>

<221> misc_feature

<222> (1)..(23)

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cagctacagc agcagtaacc atc

23

<210> 7

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      primer MAS2

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<222> (1)..(21)

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      MS1

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<221> misc_feature
<222> (1)..(22)

<400> 8
cgatggccaa gctacttctc gt 22

<210> 9
<211> 452
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(452)
<223> /note="Mouse AMCase"

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  1           5           10           15

Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro Cys Leu Cys Thr His
  20          25           30

Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn Glu Ile Thr Thr Ile
  35          40           45

Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe Asn Asp Leu Lys Asn
  50          55           60

Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe
  65          70           75           80

Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr Ser Gln Asn Arg Gln
  85          90           95

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Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Gly Phe Asp
100 105 110

Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro Pro
115 120 125

Gln Asp Lys His Leu Phe Thr Val Leu Val Lys Glu Met Arg Glu Ala
130 135 140

Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro Arg Leu Met Val Thr
145 150 155 160

Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln Ala Gly Tyr Glu Ile
165 170 175

Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His Val Met Thr Tyr Asp
180 185 190

Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu Tyr
195 200 205

Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp Tyr
210 215 220

Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro Ala Glu Lys Leu Ile
225 230 235 240

Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile Leu Arg Asn Pro Ser
245 250 255

Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp Gly Pro Ala Gly Ala
260 265 270

Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr Glu Ile Cys Thr Phe
275 280 285

Leu Arg Ser Gly Ala Thr Glu Val Trp Asp Ala Ser Gln Glu Val Pro
290 295 300

Tyr Ala Tyr Lys Ala Asn Glu Trp Leu Gly Tyr Asp Asn Ile Lys Ser
305 310 315 320

Phe Ser Val Lys Ala Gln Trp Leu Lys Gln Asn Asn Phe Gly Gly Ala
325 330 335

Met Ile Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Ser Phe Cys Asp
340 345 350

Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn Lys Ala Leu Gly Ile
355 360 365

Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro Ser Glu Pro Val Thr
370 375 380

Thr Pro Pro Gly Ser Gly Ser Gly Gly Ser Ser Gly Gly Ser Ser
385 390 395 400

Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp Gly Leu Tyr Pro Val
405 410 415

Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile Asn Gly Ile Thr Tyr
420 425 430

Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp Thr Ser Cys Asn Cys
435 440 445

Cys Asn Trp Pro
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<210> 10
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<213> Homo sapiens

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<222> (1)..(445)
<223> /note="Human chitotriosidase"

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1 5 10 15

Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp Pro Ser Leu Cys Thr His
20 25 30

Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn His Gln Leu Ser Thr Thr
35 40 45

Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu Phe Asn Gly Leu Lys Lys
50 55 60

Met Asn Pro Lys Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe
65 70 75 80

Gly Thr Gln Lys Phe Thr Asp Met Val Ala Thr Ala Asn Asn Arg Gln
85 90 95

Thr Phe Val Asn Ser Ala Ile Arg Phe Leu Arg Lys Tyr Ser Phe Asp
100 105 110

Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Gln Gly Ser Pro Ala
115 120 125

Val Asp Lys Glu Arg Phe Thr Thr Leu Val Gln Asp Leu Ala Asn Ala
130 135 140

Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys Glu Arg Leu Leu Ser
145 150 155 160

Ala Ala Val Pro Ala Gly Gln Thr Tyr Val Asp Ala Gly Tyr Glu Val
165 170 175

Asp Lys Ile Ala Gln Asn Leu Asp Phe Val Asn Leu Met Ala Tyr Asp
180 185 190

Phe His Gly Ser Trp Glu Lys Val Thr Gly His Asn Ser Pro Leu Tyr
195 200 205

Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser Leu Asn Val Asp Ala

210

215

220

Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro Ala Ser Lys Leu Ile
225 230 235 240

Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr Leu Ala Ser Ser Ser
245 250 255

Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser Gly Thr Pro Gly Pro
260 265 270

Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr Glu Val Cys Ser Trp
275 280 285

Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln Lys Val Pro Tyr Ile
290 295 300

Phe Arg Asp Asn Gln Trp Val Gly Phe Asp Asp Val Glu Ser Phe Lys
305 310 315 320

Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly Leu Gly Gly Ala Met Val
325 330 335

Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly Phe Ser Cys Asn Gln Gly
340 345 350

Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln Glu Leu Ser Leu Pro Tyr
355 360 365

Leu Pro Ser Gly Thr Pro Glu Leu Glu Val Pro Lys Pro Gly Gln Pro
370 375 380

Ser Glu Pro Glu His Gly Pro Ser Pro Gly Gln Asp Thr Phe Cys Gln
385 390 395 400

Gly Lys Ala Asp Gly Leu Tyr Pro Asn Pro Arg Glu Arg Ser Ser Phe
405 410 415

Tyr Ser Cys Ala Ala Gly Arg Leu Phe Gln Gln Ser Cys Pro Thr Gly
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Leu Val Phe Ser Asn Ser Cys Lys Cys Cys Thr Trp Asn
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24

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Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala Gln Tyr Arg Pro Gly
  1           5           10           15

Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro Cys Leu Cys Thr His
  20          25           30

Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn Glu Ile Thr Thr Ile
  35          40           45

Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe Asn Gly Leu Lys Asn
  50          55           60

Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe
  65          70           75           80

Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr Pro Glu Asn Arg Gln
  85          90           95

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Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Glu Phe Asp
100 105 110

Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro Pro
115 120 125

Gln Asp Lys His Leu Phe Thr Val Leu Val Gln Glu Met Arg Glu Ala
130 135 140

Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro Arg Leu Met Val Thr
145 150 155 160

Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln Ser Gly Tyr Glu Ile
165 170 175

Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His Val Met Thr Tyr Asp
180 185 190

Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu Tyr
195 200 205

Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp Tyr
210 215 220

Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro Ala Glu Lys Leu Ile
225 230 235 240

Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile Leu Ser Asn Pro Ser
245 250 255

Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala Gly Pro Ala Gly Pro
260 265 270

Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr Glu Ile Cys Thr Phe
275 280 285

Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala Pro Gln Glu Val Pro
290 295 300

Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr Asp Asn Ile Lys Ser
305 310 315 320

Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn Lys Phe Gly Gly Ala
325 330 335

Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Thr Phe Cys Asn
340 345 350

Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys Lys Ala Leu Gly Leu
355 360 365

Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro Ile Glu Pro Ile Thr
370 375 380

Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly Ser Ser Ser Ser Gly
385 390 395 400

Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val Arg Ala Asn Gly Leu
405 410 415

Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp His Cys Val Asn Gly
420 425 430

Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu Val Phe Asp Thr Ser
435 440 445

Cys Asp Cys Cys Asn Trp Ala
450 455